

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Timothy A
Rosen, Craig
- (ii) TITLE OF INVENTION: Endothelial-Monocyte Activating
Polypeptide III
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
- (B) STREET: 6 BECKER FARM ROAD
- (C) CITY: ROSELAND
- (D) STATE: NEW JERSEY
- (E) COUNTRY: USA
- (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/483,534
- (B) FILING DATE: 07 JUN 95
- (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: MULLINS, J.G.
- (B) REGISTRATION NUMBER: 33,073
- (C) REFERENCE/DOCKET NUMBER: 325800-464 (PF206)
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 636 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TACCCCTGCC CTGAAAAAAC TGGCCAGCGC TGCCTACCCA GATCCCTCAA AGCAGAAGCC 60
AATGGCCAAA GGCCTGCCAA GAATTCAGAA CCA GAG GAG GTC ATC CCA TCC CGG 114
Glu Glu Val Ile Pro Ser Arg
1 5
CTG GAT ATC CGT GTG GGG AAA ATC ATC ACT GTG GAG AAG CAC CCA GAT 162
Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp
10 15 20
GCA GAC AGC CTG TAT GTA GAG AAG ATT GAC GTG GGG GAA GCT GAA CCA 210
Ala Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro
25 30 35
CGG ACT GTG GTG AGC GGC CTG GTA CAG TTC GTG CCC AAG GAG GAA CTG 258
Arg Thr Val Val Ser Gly Leu Val Gln Phe Val Pro Lys Glu Glu Leu
40 45 50 55
CAG GAC AGG CTG GTA GTG GTG CTG TGC AAC CTG AAA CCC CAG AAG ATG 306
Gln Asp Arg Leu Val Val Leu Cys Asn Leu Lys Pro Gln Lys Met
60 65 70
AGA GGA GTC GAG TCC CAA GGC ATG CTT CTG TGT GCT TCT ATA GAA GGG 354
Arg Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly
75 80 85
ATA AAC CGC CAG GTT GAA CCT CTG GAC CCT CCG GCA GGC TCT GCT CCT 402
Ile Asn Arg Gln Val Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala Pro
90 95 100
GGT GAG CAC GTG TTT GTG AAG GGC TAT GAA AAG GGC CAA CCA GAT GAG 450
Gly Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu
105 110 115
GAG CTC AAG CCC AAG AAG AAA GTC TTC GAG AAG TTG CAG GCT GAC TTC 498
Glu Leu Lys Pro Lys Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe
120 125 130 135
AAA ATT TCT GAG GAG TGC ATC GCA CAG TGG AAG CAA ACC AAC TTC ATG 546
Lys Ile Ser Glu Glu Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met
140 145 150
ACC AAG CTG GGC TCC ATT TCC TGT AAA TCG CTG AAA GGG GGG AAC ATT 594
Thr Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile
155 160 165
AGC TAG CCAGCCCAGC ATCTTCCCCC CTTCTTCCAC CACTGA 636
Ser

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 168 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile
5 10 15
Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu Lys Ile
20 25 30
Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu Val Gln
35 40 45
Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val Leu Cys
50 55 60
Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly Met Leu
65 70 75 80
Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro Leu Asp
85 90 95
Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys Gly Tyr
100 105 110
Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Lys Val Phe
115 120 125
Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile Ala Gln
130 135 140
Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser Cys Lys
145 150 155 160
Ser Leu Lys Gly Gly Asn Ile Ser
165

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCGGATCC GAGGAGGTCA TCCCATCC

28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCAAGCTT CTAGATAATG TTCCCCC

28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCGGATCC GAGGAGGTCA TCCCATCC

28

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCAAGCTT CTAGATAATG TTCCCCC

28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 183 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys	Gly	Glu	Lys	Lys	Glu	Lys	Lys	Gln	Gln	Ser	Ile	Ala	Gly	Ser	
				5					10					15	
Ala	Asp	Ser	Lys	Pro	Ile	Asp	Val	Ser	Arg	Leu	Asp	Leu	Arg	Ile	
				20					25					30	
Gly	Cys	Ile	Ile	Thr	Ala	Arg	Lys	His	Pro	Asp	Ala	Asp	Ser	Leu	
				35					40					45	
Tyr	Val	Glu	Glu	Val	Asp	Val	Gly	Glu	Ile	Ala	Pro	Arg	Thr	Val	
				50					55					60	
Val	Ser	Gly	Leu	Val	Asn	His	Val	Pro	Leu	Glu	Gln	Met	Gln	Asn	
				65					70					75	
Arg	Met	Val	Ile	Leu	Leu	Cys	Asn	Leu	Lys	Pro	Ala	Lys	Met	Arg	
				80					85					90	
Gly	Val	Lys	Ser	Gln	Ala	Met	Val	Met	Cys	Ala	Ser	Ser	Pro	Glu	
				95					100					105	
Lys	Ile	Glu	Ile	Leu	Ala	Pro	Pro	Asn	Gly	Ser	Val	Pro	Gly	Asp	
				110					115					120	
Arg	Ile	Thr	Phe	Asp	Ala	Phe	Pro	Gly	Glu	Pro	Asp	Lys	Glu	Lys	
				125					130					135	
Asn	Pro	Lys	Lys	Lys	Ile	Trp	Glu	Gln	Ile	Gln	Pro	Asp	Leu	His	
				140					145					150	
Thr	Asn	Asp	Glu	Cys	Val	Ala	Thr	Tyr	Lys	Glu	Val	Pro	Phe	Glu	
				155					160					165	
Val	Lys	Gly	Lys	Gly	Val	Cys	Arg	Ala	Gln	Thr	Met	Ser	Asn	Ser	
				170					175					180	
Gly	Ile	Lys													

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